Remarks

Claims 1, 7-16, 19-21, 30-37, 39-48 and 52-54 were pending. Claims 34-47 and 52-53 are cancelled. No new claims are added. Claim 1 is amended. Therefore, claims 1, 7-16, 19-21, 30-33, 48 and 54 are now pending.

Specification

The specification was amended to correctly refer to Figure 3 on page 32 at lines 18-19. Therefore, Applicant requests that the objection to the specification be withdrawn.

35 U.S.C. § 112, first paragraph

Claims 1, 7-16, 19-21, 30-37, 39-48 and 52-54 were rejected under 35 U.S.C. § 112, first paragraph on the grounds that the claims were not adequately described in the specification. Applicant disagrees because methods which allow one skilled in the art to generate such variant sequences, and determine the promoter activity of the variant sequences, are provided in the specification (for example, see page 19, line 1 – page 21, line 21; page 25, line 25- page 29, line 26). However, in order to expedite prosecution of the present application, the claims are now directed to sequences which comprise bases 398-853 of SEQ ID NO: 17, which the Examiner stated is enabled (paragraph 5 on page 5 of the Office action). Therefore, Applicant requests that the 35 U.S.C. § 112, first paragraph rejection with respect to sequence identity and fragments be withdrawn.

Claims 1, 7-16, 19-21, 30-37, 39-48 and 52-54 were also rejected under 35 U.S.C. § 112, first paragraph on the grounds that the claims were not adequately described in the specification, because the Applicant only showed that the constructs had promoter activity in Douglas-fir seeds, and thus it would require undue experimentation to determine which host cells in which the constructs function as promoters. Applicant disagrees because the specification teaches one skilled in the art how to make and test variant sequences for promoter activity (for example, see page 19, line 1 – page 21, line 21; page 25, line 25- page 29, line 26). Therefore, it does not require undue experimentation to make and use the claimed invention in its full scope.

In addition, Applicant has provided herein a Declaration, signed by a post-doctoral fellow in her laboratory, Dr. Milian Osusky. The data presented in the Declaration (FIGS. 1 and 2), was generated using methods enabled in the specification (for example see page 19, line 1 – page 21,

line 21; page 32, line 18- page 33, line 16; and page 34, lines 10-32). The data shown in FIGS. 1 and 2 demonstrate that SEQ ID NO: 17 functions as a promoter in tobacco plants, as do fragments which contain nucleotides 398-853 or 180-853 of SEQ ID NO: 17. Therefore, Applicant should not be limited to promoter activity in Douglas Fir.

Applicant therefore requests that he 35 U.S.C. § 112, first paragraph rejection with respect to undue experimentation be withdrawn.

35 U.S.C. § 112, second paragraph

Claims 1, 7-16, 19-21, 30-37, 39-48 and 52-54 were rejected under 35 U.S.C. § 112, second paragraph on the grounds that the phrase "capable of driving the expression of a transgene" is not definite. Applicants disagree and request reconsideration. The fact that a non-promoter sequence may be capable of driving expression of a transgene is not relevant. The claims are to a promoter sequence (particularly one that includes nucleotides 398-853 of SEQ ID NO: 17) which can drive transcription (see page 12, line 29- page 13, line 3). As Applicant is allowed to be her own lexicographer, this 35 U.S.C. § 112, second paragraph rejection is improper, and Applicant requests that it be withdrawn.

If there are any questions, the Examiner is invited to telephone the undersigned at the telephone number listed below.

Respectfully submitted,

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Marked-up Version of Amended Claims and Specification Pursuant to 37 C.F.R. §§ 1.121(b)-(c)

Teplace the paragraph on page 32, lines 18-27 of the specification with the following:

Douglas-fir gene promoter-GUS chimeric constructs as shown in Figure[s 20 and 38] 3 were constructed. For construction of pMTP0.9-GUS, the 0.9-kb fragment of the 5'-flanking sequence of the *gPmMTa* gene was PCR-amplified from the plasmid gPMMTa-Exo1.2 using a pair of primers, creating *PstI/SalI* sites at 5'-end and *XbaI/Bam*HI sites at 3'-end of the promoter fragment. After partial digestion with *XbaI/Pst*I, the 0.96-kb PCR product was cloned into pBI221 vector (Clontech, Palo Alto, California) in place of the *XbaI/Pst*I fragment of the CaMV 35S promoter region. For construction of pMTP0.2, the plasmid pMTP0.9 was partially digested with *Hind*III/*Xba*I, and the isolated 0.28-kb fragment was cloned into pBI221 vector, thereby replacing the *Hind*III/*Xba*I fragment of the CaMV 35S promoter region.

In the Claims:

1. (Thrice Amended) A recombinant promoter, capable of driving expression of a transgene operably linked to the promoter, wherein the promoter comprises [a nucleic acid sequence that shares at least 80% sequence identity to] nucleotides [667-853] 398-853 of SEQ ID NO: 17.

34. (Cancel) [The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 90% sequence identity to nucleotides 667-853 of SEQ ID NO: 17.]

35. (Cancel) [The promoter of claim 1, wherein the promoter comprises nucleotides 667-853 of SEQ ID NO: 17.]

36. (Cancel) [The promoter of claim 1, wherein the promoter comprises at least 20 consecutive nucleic acid residues of a nucleic acid sequence sharing at least 80% sequence identity to nucleotides 667-853 of SEQ ID NO: 17.]

37. (Cancel) [The promoter of claim 1, wherein the promoter comprises at least 20 consecutive nucleic acid residues of nucleotides 667-853 of SEQ ID NO: 17.]

39. (Cancel) [The promoter of claim 1, wherein the promoter comprises at least 40 consecutive nucleic acid residues of a nucleic acid sequence sharing at least 90% sequence identity to nucleotides 667-853 of SEQ ID NO: 17.]

40. (Cancel) [The promoter of claim 1, wherein the promoter comprises at least 40 consecutive nucleic acid residues of nucleotides 667-853 of SEQ ID NO: 17.]

41. (Cancel) [The promoter of claim 1, wherein the promoter comprises at least 60 consecutive nucleic acid residues of a nucleic acid sequence sharing at least 90% sequence identity to nucleotides 667-853 of SEQ ID NO: 17.]

42. (Cancel) [The promoter of claim 1, wherein the promoter comprises at least 60 consecutive nucleic acid residues of nucleotides 667-853 of SEQ ID NO: 17.]

43. (Cancel) [The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 80% sequence identity to nucleotides 398-853 of SEQ ID NO: 17.]

44. (Cancel) [The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 90% sequence identity to nucleotides 398-853 of SEQ ID NO: 17.]

45. (Cancel) [The promoter of claim 1, wherein the promoter comprises nucleotides 398-853 of SEQ ID NO: 17.]

46. (Cancel) [The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 80% sequence identity to nucleotides 180-853 of SEQ ID NO: 17.]

47. (Cancel) [The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 90% sequence identity to nucleotides 180-853 of SEQ ID NO: 17.]

52. (Cancel) [The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 80% sequence identity to SEQ ID NO: 17.]

53. (Cancel) [The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 17.]